

SEQUENCE ID LISTING

SEQ ID NO: 1 is the amino acid sequence of residues 33-79 of c-Jun.

SEQ ID NO: 2 is the nucleotide sequence for an N-terminal primer used for producing c-Jun truncation mutants.

- 5 SEQ ID NO: 3 is the nucleotide sequence for an N-terminal primer used for producing c-Jun truncation mutants.

SEQ ID NO: 4 is the nucleotide sequence for an N-terminal primer used for producing c-Jun truncation mutants.

- 10 SEQ ID NO: 5 is the nucleotide sequence for an N-terminal primer used for producing c-Jun truncation mutants.

SEQ ID NO: 6 is the nucleotide sequence for an N-terminal primer used for producing c-Jun truncation mutants.

SEQ ID NO: 7 is the nucleotide sequence for a C-terminal primer used for producing c-Jun truncation mutants.

- 15 SEQ ID NO: 8 is the nucleotide sequence for a C-terminal primer used for producing c-Jun truncation mutants.

SEQ ID NO: 9 is the nucleotide sequence and deduced amino acid sequence for *c-jun* and c-Jun.

SEQ ID NO: 10 is the deduced amino acid sequence of c-Jun.

08799913-021397
465720-ET65280

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Karin, Michael
Hibi, Masahiko
Lin, Anning

(ii) TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE: 18 JUL-1994
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Wetherell, Jr., Ph.D., John R.,
(B) REGISTRATION NUMBER: 31,678
(C) REFERENCE/DOCKET NUMBER: PD-3701

(ix) TELECOMMUNICATION INFORMATION:

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1994-07-20 10:00:00

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: c-Jun/JNK binding site

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..47

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ile	Leu	Lys	Gln	Ser	Met	Thr	Leu	Asn	Leu	Ala	Asp	Pro	Val	Gly	Ser
1				5					10					15	
Leu	Lys	Pro	His	Leu	Arg	Ala	Lys	Asn	Ser	Asp	Leu	Leu	Thr	Ser	Pro
			20					25					30		
Asp	Val	Gly	Leu	Leu	Lys	Leu	Ala	Ser	Pro	Glu	Leu	Glu	Arg	Leu	
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: N-terminal primer

08799913.021397

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5 TCTGCAGGAT CCCCATGACT GCAAAGATGG AAACG

35

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: N-terminal primer

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCTGCAGGAT CCCCGACGAT GCCCTCAACG CCTC

34

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: N-terminal primer

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(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

5 TCTGCAGGAT CCCCAGAGAGC GGACCTTATG GCTAC

35

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: N-terminal primer

15

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCTGCAGGAT CCCC GCCGAC CCAGTGGGGA GCCTG

35

20 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: N-terminal primer

26ET20"ET66480

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

5 TCTGCAGGAT CCCCAAGAAC TCGGACCTCC TCACC

35

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: C-terminal primer

15 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGAATTCCTGC AGGCGCTCCA GCTCGGGCGA

30

20 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: C-terminal primer

269913-01397

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

5 TGAATTCCTG CAGGTCGGCG TGGTGGTGAT GTG

33

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2096 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: Jun

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 412..1404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCGGGG GCGGCCAAGA CCCGCCGCCG GCCGGCCACT GCAGGGTCCG CACTGATCCG 60

20 CTCCGGCGGA GAGCCGCTGC TCTGGAAGT CAGTTCGCCT GCGGACTCCG AGGAACCGCT 120

GCGCACGAAG AGCCGTCAGT GAGTGACCGC GACTTTTCAA AGCCGGGTAG GGCGCGCGAG 180

TCGACAAGTA AGAGTGCGGG AGGCATCTTA ATTAACCCTG CGCTCCCTGG AGCAGCTGGT 240

GAGGAGGGCG CACGGGGACG ACAGCCAGCG GGTGCGTGCG CTCTTAGAGA AACTTTCCCT 300

GTCAAAGGCT CCGGGGGGCG CGGGTGTCCC CCGCTTGCCA CAGCCCTGTT GCGGCCCCGA 360

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	AACTTGTGCG CGCAGGCCAA ACTAACCTCA CGTGAAGTGA CGGACTGTC T ATG ACT	417
	Met Thr 1	
5	GCA AAG ATG GAA ACG ACC TTC TAT GAC GAT GCC CTC AAC GCC TCG TTC Ala Lys Met Glu Thr Thr Phe Tyr Asp Asp Ala Leu Asn Ala Ser Phe 5 10 15	465
	CTC CCC TCC GAG AGG GGA CCT TAT GGC TAC AGT AAC CCC AAG ATC CTG Leu Pro Ser Glu Arg Gly Pro Tyr Gly Tyr Ser Asn Pro Lys Ile Leu 20 25 30	513
10	AAA CAG AGC ATG ACC CTG AAC CTG GCC GAC CCA GTG GGG AGC CTG AAG Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser Leu Lys 35 40 45 50	561
15	CCG CAC CTC CGC GCC AAG AAC TCG GAC CTC CTC ACC TCG CCC GAC GTG Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro Asp Val 55 60 65	609
	GGG CTG CTC AAG CTG GCG TCG CCC GAG CTG GAG CGC CTG ATA ATC CAG Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu Ile Ile Gln 70 75 80	657
20	TCC AGC AAC GGG CAC ATC ACC ACC ACG CCG ACC CCC ACC CAG TTC CTG Ser Ser Asn Gly His Ile Thr Thr Thr Pro Thr Pro Thr Gln Phe Leu 85 90 95	705
	TGC CCC AAG AAC GTG ACA GAT GAG CAG GAG GGG TTC GCC GAG GGC TTC Cys Pro Lys Asn Val Thr Asp Glu Gln Glu Gly Phe Ala Glu Gly Phe 100 105 110	753
25	GTG CGC GCC CTG GCC GAA CTG CAC AGC CAG AAC ACG CTG CCC AGC GTC Val Arg Ala Leu Ala Glu Leu His Ser Gln Asn Thr Leu Pro Ser Val 115 120 125 130	801
30	ACG TCG GCG GCG CAG CCG GTC AAC GGG GCA GGC ATG GTG GCT CCC GCG Thr Ser Ala Ala Gln Pro Val Asn Gly Ala Gly Met Val Ala Pro Ala 135 140 145	849
	GTA GCC TCG GTG GCA GGG GGC AGC GGC AGC GGC GGC TTC AGC GCC AGC Val Ala Ser Val Ala Gly Gly Ser Gly Ser Gly Gly Phe Ser Ala Ser 150 155 160	897
	CTG CAC AGC GAG CCG CCG GTC TAC GCA AAC CTC AGC AAC TTC AAC CCA	945

26ET20-ET566480

[illegible]

CCGACGGAGA GAAAAAAGAA GTGTCCGAGA ACTAAAGCCA AGGGTATCCA AGTTGGACTG 1544
GGTTCGGTCT GACGGCGCCC CCAGTGTGCA CGAGTGGGAA CCACCTGGTC GCGCCCTCCC 1604
TTGGCGTCGA GCCAGGGAGC GGCCGCCTGG GGGCTGCCCC GCTTTCGGGA CGGGCTGTCC 1664
CCGCGCGAAC GGAACGTTGG ACTTTCGTTA ACATTGACCA AGAACTGCAT GGACCTAACA 1724
5 TTCGATCTCA TTCAGTATTA AAGGGGGCAG GGGGAGGGGG TTACAAACTG CAATAGAGAC 1784
TGTAGATTGC TTCTGTAGTA CTCCTTAAGA ACACAAAGCG GGGGGAGGGT TGGGGAGGGG 1844
CGGCAGGAGG GAGGTTTGTG AGAGCGAGGC TGAGCCTACA GATGAACTCT TTCTGGCCTG 1904
CTTTCGTAA CTGTGTATGT ACATATATAT ATTTTAAAT TTGATTAAAG CTGATTACTG 1964
TCAATAAACA GCTTCATGCC TTGTAAAGTT ATTTCTTGTG TGTGTTTGG GGATCCTGCC 2024
10 CAGTGTGTT TGTAATAAG AGATTGGAG CACTCTGAGT TTACCATTG TAATAAAGTA 2084
TATAATTTTT TT 2096

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

20 Met Thr Ala Lys Met Glu Thr Thr Phe Tyr Asp Asp Ala Leu Asn Ala
1 5 10 15
Ser Phe Leu Pro Ser Glu Arg Gly Pro Tyr Gly Tyr Ser Asn Pro Lys
20 25 30
Ile Leu Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser
35 40 45
25 Leu Lys Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro
50 55 60

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	Asp	Val	Gly	Leu	Leu	Lys	Leu	Ala	Ser	Pro	Glu	Leu	Glu	Arg	Leu	Ile	
	65					70					75					80	
	Ile	Gln	Ser	Ser	Asn	Gly	His	Ile	Thr	Thr	Thr	Pro	Thr	Pro	Thr	Gln	
					85					90					95		
5	Phe	Leu	Cys	Pro	Lys	Asn	Val	Thr	Asp	Glu	Gln	Glu	Gly	Phe	Ala	Glu	
				100					105					110			
	Gly	Phe	Val	Arg	Ala	Leu	Ala	Glu	Leu	His	Ser	Gln	Asn	Thr	Leu	Pro	
			115					120					125				
10	Ser	Val	Thr	Ser	Ala	Ala	Gln	Pro	Val	Asn	Gly	Ala	Gly	Met	Val	Ala	
	130						135					140					
	Pro	Ala	Val	Ala	Ser	Val	Ala	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Phe	Ser	
	145					150					155					160	
	Ala	Ser	Leu	His	Ser	Glu	Pro	Pro	Val	Tyr	Ala	Asn	Leu	Ser	Asn	Phe	
					165					170					175		
15	Asn	Pro	Gly	Ala	Leu	Ser	Ser	Gly	Gly	Gly	Ala	Pro	Ser	Tyr	Gly	Ala	
				180					185					190			
	Ala	Gly	Leu	Ala	Phe	Pro	Ala	Gln	Pro	Gln	Gln	Gln	Gln	Gln	Pro	Pro	
			195					200					205				
20	His	His	Leu	Pro	Gln	Gln	Met	Pro	Val	Gln	His	Pro	Arg	Leu	Gln	Ala	
	210						215					220					
	Leu	Lys	Glu	Glu	Pro	Gln	Ile	Val	Pro	Glu	Met	Pro	Gly	Glu	Thr	Pro	
	225					230					235					240	
	Pro	Leu	Ser	Pro	Ile	Asp	Met	Glu	Ser	Gln	Glu	Arg	Ile	Lys	Ala	Glu	
					245					250					255		
25	Arg	Lys	Arg	Met	Arg	Asn	Arg	Ile	Ala	Ala	Ser	Lys	Cys	Arg	Lys	Arg	
				260					265					270			
	Lys	Leu	Glu	Arg	Ile	Ala	Arg	Leu	Glu	Glu	Lys	Val	Lys	Thr	Leu	Lys	
			275					280					285				
30	Ala	Gln	Asn	Ser	Glu	Leu	Ala	Ser	Thr	Ala	Asn	Met	Leu	Arg	Glu	Gln	
	290						295					300					

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Val Ala Gln Leu Lys His Lys Val Met Asn His Val Asn Ser Gly Cys
305 310 315 320

Gln Leu Ile Leu Thr Gln Gln Leu Gln Thr Phe
325 330

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